In re Application of:
Short
Application No.: 09/594,459
Filed: June 14, 2000

PATENT
Attorney Docket No.: DIVER1460-15

I. AMENDMENTS

A. In the Specification

At page 63, line 21, please delete "1006" and replace with --100^6--

B. In the Claims

Please cancel claims 1 and 2 without prejudice, and enter claims 3-14 as follows. The Applicant respectfully submits that the present amendments do not narrow the scope of the claimed invention or surrender the subject matter of the invention in any way. Specifically, the Applicant respectfully submits that present amendments present no narrowing to meet any statutory requirement - either voluntarily or to overcome or to distinguish the claimed invention from any prior art; thus, the patent claims submitted herein are therefore not subject to the creation of a prosecution history estoppel as described, e.g. in Festo Corp. v. Shoketsu Kinzoku Kogyo Kabushiki Co., Ltd., 234 F.3d 558, 56 U.S.P.Q.2d 1865 (Fed.Cir. 2000).

--3. A method of producing a progeny library comprised of chimerized but pre-determined polynucleotide sequences each of which is comprised of a pre-determined number of building block sequences that are assembled in non-random order, the method comprising:

(a) generating a plurality of pre-determined nucleic acid building block sequences comprised of sequences delineated by demarcation points selected from aligned progenitor nucleic acid sequences; and

(b) non-stochastically assembling said nucleic acid building block sequences to produce said chimerized but pre-determined polynucleotide sequences, such that a designed overall assembly order is achieved for each of said chimerized but pre-determined polynucleotide sequences.

4. The method of claim 3 where the progenitor nucleic acid sequences comprise sequences derived from an uncultivated organism or an environmental sample.

In re Application of:
Short
Application No.: 09/594,459
Filed: June 14, 2000

PATENT
Attorney Docket No.: DIVER1460-15

5. 3 The method of claim 1 where the progenitor nucleic acid sequences are comprised of genomic nucleic acid sequences.

6. 4 The method of claim 1, where the progeny library is comprised of at least 10^{10} different pre-determined progeny molecular sequences.

7. 5 The method of claim 1, where the progeny library is comprised of at least 10^{15} different pre-determined progeny molecular sequences.

8. 6 The method of any of claim 1-5, where the nucleic acid building block sequences are obtained from polynucleotide sequences that encode enzymes or fragments thereof.

9. 7 The method of any of claim 1-5, where the nucleic acid building block sequences are assembled to produce polynucleotides encoding biochemical pathways from one or more operons or gene clusters of portions thereof.

10. 8 The method of any of claim 1-5, where the nucleic acid building block sequences are obtained from polynucleotides encoding polyketides or fragments thereof.

11. 9 The method of any of claim 1-5, where the nucleic acid building block sequences are obtained from polynucleotides encoding antibodies or antibody fragments or other peptides or polypeptides.

bicarcid.

12. 10 The method of any of claim 1-5, where the step of (b) non-stochastically assembling said nucleic acid building blocks is performed to generate a display library comprised of polypeptides or antibodies or peptidomimetic antibodies or antibody variable region sequences suitable for affinity interaction screening.

13. 11 The method of any of claim 1-5, further comprising the step of:
(c) screening said progeny library to identify an evolved molecular property.

14. 12 The method of claim 13, where step of (c) is comprised of expression screening to identify an evolved molecular property.--